NEURONAL and RETINAL GENE EXPRESSION PATTERNS

ABSTRACT

The retinal degeneration (*rd1*) mutant mouse exhibits rapid rod photoreceptor degeneration caused by a mutation in the rod photoreceptor-specific gene cGMP phosphodiesterase β (PDE). One intriguing aspect of the *rd1* phenotype is a secondary wave of cone photoreceptor death that follows loss of rods. In this study, we investigated gene expression changes associated with the progression of photoreceptor degeneration in *rd1* mice using a custom retina microarray. The microarray contains 5,376 DNA fragments that correspond to mouse genes known or postulated to be involved in normal retinal function, development, or disease. Gene expression in *rd1* retina was compared with age-matched wild-type controls at three time-points corresponding to critical stages in retina degeneration: peak of rod degeneration, early in cone degeneration and during cone degeneration. Statistical significance analyses demonstrated that approximately 3% of the genes on the microarray were differentially expressed, including known genes and genes that had not been previously implicated in degeneration. Interestingly, there was less overlap in the genes that were upregulated at each stage of degeneration, suggesting the involvement of distinct molecular pathways. Genes involved in transport, signalling and cytoskeleton were differentially expressed during rod degeneration whereas genes involved in growth and proliferation, oxidative stress and protein modification were increased prior to and during cone degeneration. These results provide clues to underlying molecular processes occurring during photoreceptor degeneration, and provide direction for future cell-based studies.